

Serial Number:

09/900,518A

CRF Processing Date: 5/31/02

Edited by: M. SPENCER

Verified by: (STIC sta

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

#10

☐

Edited a format error in the Current Application Data section, specifically:

ENTERED

☐

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☒

Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as

☐

Inserted mandatory headings, specifically:

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

☐

Other:

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING

DATE: 05/31/2002

PATENT APPLICATION: US/09/900,518A

TIME: 14:04:00

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\05312002\I900518A.raw

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4 <110> APPLICANT: Allen, Keith D.
5   Zhang, Qin
7 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CX2 GENE
8   DISRUPTIONS
10 <130> FILE REFERENCE: R-716
12 <140> CURRENT APPLICATION NUMBER: US 09/900,518A
13 <141> CURRENT FILING DATE: 2001-07-06
15 <150> PRIOR APPLICATION NUMBER: US 60/216,178
16 <151> PRIOR FILING DATE: 2000-07-06
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2490
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
27 <400> SEQUENCE: 1
28 aggctgtccc acccaccate tgcacccgct gcagcgcccg cgcccctgtc ccgcgcgcta 60
29 gtcgtcatTT gtagcccgcc tgccgctccc ggggacccga tccctaccctg ggtgcggggc 120
30 agagcgggca tggcccgctc ggggaccgcc tgccctgcgc tggcgctggc cctggcactt 180
31 gtggcggttg ccctggctgg agtcagagcc cagggcgagc ccttcgagga gcctgactat 240
32 tacagccagg agctctggcg gcgcggggcg tattatgggc atccggagcc tgagccggag 300
33 ccggagctct tctgccttc aatgcatgaa gacctagggt tggaggagca ggaacagcag 360
34 gagccgcacc agcagggcc aagaactccc aagaaggcca tcaagcccaa gaaggctccc 420
35 aagagggaga agttagtgtc agagacgcct ccaccaggta aaaatagcaa cagaaaaggc 480
36 agaagaagca agaactctga gaaagctgcc agtgatgacc atggtgtccc tgtggctcat 540
37 gaggatgtca gagagagttg cccacctctt ggtctggaaa cattaataat cacagacttc 600
38 cagctgcatg cctccacatc gaagcggtat ggctgggag cccaccgggg gagactcaac 660
39 atccaggcag gcattaatga aaatgacttt tacgatgggg ctgtgtgtgc tggtaggaac 720
40 gacttgcatc agtggatcga agtggatgcc cggcgccctga ccaagtccac aggggtcatt 780
41 acccaaggaa ggaactctct ctggctgagt gactgggtga catcctataa agtcatggtg 840
42 agcaatgaca gccacacatg ggttactgtg aagaatggat ctggcgacat gatatttgaa 900
43 ggaaacagtg agaaggagat tcctgtgctc aatgagctgc cagtcccatc ggtggcccg 960
44 tacattcgca taaacctca gtccctggtt gataacggga gcatctgcat gaggatggag 1020
45 atcttgggct gccactgcc ggatccta aactattatc accgacgtaa tgagatgacc 1080
46 accacggatg acctggattt taagcaccac aactataagg aaatgcgcca gttgatgaag 1140
47 gttgtcaatg aaatgtgccc caatattacc aggatttaca acattggcaa aagccaccag 1200
48 ggcctgaaat tgtatgcggt agagatctct gaccatcctg gggaacatga agttggtgag 1260
49 ccgaggttcc actacatcgc agggggccac ggcaatgagg ttctgggacg agaactgctg 1320
50 ctgctgctgc tgcaacttct ctgccaggaa tactcggcgc agaacgcacg catcgtccgc 1380
51 ttggtggagg agactcgaat ccacattcta ccctccctca atcctgatgg ctatgagaag 1440
52 gcctatgaag gaggttccga gttgggaggc tggctccctg gacgttggac ccatgatggc 1500
53 atcgatatca acaacaactt tccggattta aactcgctgc tctgggaggc agaggaccag 1560
54 cagaatgccc caaggaaggt cccaaccac tacattgcca tccctgagtg gtttctgtct 1620

```

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```

55 gagaatgcca cagtggccac agagaccaga gccgtcatcg cctggatgga gaagatcccg 1680
56 tttgtgctgg gaggcaacct acaggggggt gagctggctg tggcataccc ctatgacatg 1740
57 gtgcggtccc tgtggaagac ccaggagcac accccaacac ctgatgatca tgtgttccgc 1800
58 tggctggcgt attcctacgc ctccactcac cgcctcatga cagatgccag gaggcgagtg 1860
59 tgccacacgg aagattttca gaaggaggag ggcaccgtca atggggcttc ctggcacaca 1920
60 gtggctggaa gtctaaacga ttccagctac ctccatacaa actgctttga gctgtccatc 1980
61 tacgtgggct gtgataaata cccacacgag agcgagctgc cggaggaatg ggagaataac 2040
62 cgggagtgctc tgattgtgtt catggagcag gtccatcgag gcatcaaagg catagtgaga 2100
63 gatttacaag ggaaagggat ttcaaagtct gtcattctctg tggaagggtg taaccatgac 2160
64 atccggacag ccagcgatgg ggattactgg cgtctactga accctggcga atatgtggtc 2220
65 acagccaagg cggaaggctt tatcacttcc accaagaact gcatggttgg ctatgatatg 2280
66 ggagctactc ggtgtgactt caccctcaca aagaccaacc tggctaggat aagagaaatt 2340
67 atggagacat ttgggaagca gcctgtcagc ctaccctcca ggcgcctgaa gctgcgggga 2400
68 cggaaaaggc ggcagcgtgg gtgaccctgt cggacacttg agacataccc cagaccgtgc 2460
69 aaataaaaat ccactccagt agtaaaaaaa 2490

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71 <210> SEQ ID NO: 2

72 <211> LENGTH: 764

73 <212> TYPE: PRT

74 <213> ORGANISM: Mus musculus

76 <400> SEQUENCE: 2

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77 Met Ala Arg Leu Gly Thr Ala Cys Pro Ala Leu Ala Leu Ala Leu Ala
78 1 5 10 15
79 Leu Val Ala Val Ala Leu Ala Gly Val Arg Ala Gln Gly Ala Ala Phe
80 20 25 30
81 Glu Glu Pro Asp Tyr Tyr Ser Gln Leu Trp Arg Arg Gly Arg Tyr
82 35 40 45
83 Tyr Gly His Pro Glu Pro Glu Pro Glu Leu Phe Ser Pro Ser
84 50 55 60
85 Met His Glu Asp Leu Arg Val Glu Glu Gln Glu Gln Gln Glu Pro His
86 65 70 75 80
87 Gln Gln Gly His Arg Thr Pro Lys Lys Ala Ile Lys Pro Lys Lys Ala
88 85 90 95
89 Pro Lys Arg Glu Lys Leu Val Ala Glu Thr Pro Pro Pro Gly Lys Asn
90 100 105 110
91 Ser Asn Arg Lys Gly Arg Arg Ser Lys Asn Leu Glu Lys Ala Ala Ser
92 115 120 125
93 Asp Asp His Gly Val Pro Val Ala His Glu Asp Val Arg Glu Ser Cys
94 130 135 140
95 Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln Leu His
96 145 150 155 160
97 Ala Ser Thr Ser Lys Arg Tyr Gly Leu Gly Ala His Arg Gly Arg Leu
98 165 170 175
99 Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr Asp Gly Ala Trp
100 180 185 190
101 Cys Ala Gly Arg Asn Asp Leu His Gln Trp Ile Glu Val Asp Ala Arg
102 195 200 205
103 Arg Leu Thr Lys Phe Thr Gly Val Ile Thr Gln Gly Arg Asn Ser Leu
104 210 215 220
105 Trp Leu Ser Asp Trp Val Thr Ser Tyr Lys Val Met Val Ser Asn Asp

```

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```

106 225                230                235                240
107 Ser His Thr Trp Val Thr Val Lys Asn Gly Ser Gly Asp Met Ile Phe
108                245                250                255
109 Glu Gly Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val
110                260                265                270
111 Pro Met Val Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp
112                275                280                285
113 Asn Gly Ser Ile Cys Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro
114                290                295                300
115 Asp Pro Asn Asn Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Thr Asp
116 305                310                315                320
117 Asp Leu Asp Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met
118                325                330                335
119 Lys Val Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile
120                340                345                350
121 Gly Lys Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp
122                355                360                365
123 His Pro Gly Glu His Glu Val Gly Glu Pro Glu Phe His Tyr Ile Ala
124                370                375                380
125 Gly Ala His Gly Asn Glu Val Leu Gly Arg Glu Leu Leu Leu Leu Leu
126 385                390                395                400
127 Leu His Phe Leu Cys Gln Glu Tyr Ser Ala Gln Asn Ala Arg Ile Val
128                405                410                415
129 Arg Leu Val Glu Thr Arg Ile His Ile Leu Pro Ser Leu Asn Pro
130                420                425                430
131 Asp Gly Tyr Glu Lys Ala Tyr Glu Gly Gly Ser Glu Leu Gly Gly Trp
132                435                440                445
133 Ser Leu Gly Arg Trp Thr His Asp Gly Ile Asp Ile Asn Asn Asn Phe
134                450                455                460
135 Pro Asp Leu Asn Ser Leu Leu Trp Glu Ala Glu Asp Gln Gln Asn Ala
136 465                470                475                480
137 Pro Arg Lys Val Pro Asn His Tyr Ile Ala Ile Pro Glu Trp Phe Leu
138                485                490                495
139 Ser Glu Asn Ala Thr Val Ala Thr Glu Thr Arg Ala Val Ile Ala Trp
140                500                505                510
141 Met Glu Lys Ile Pro Phe Val Leu Gly Gly Asn Leu Gln Gly Gly Glu
142                515                520                525
143 Leu Val Val Ala Tyr Pro Tyr Asp Met Val Arg Ser Leu Trp Lys Thr
144                530                535                540
145 Gln Glu His Thr Pro Thr Pro Asp Asp His Val Phe Arg Trp Leu Ala
146 545                550                555                560
147 Tyr Ser Tyr Ala Ser Thr His Arg Leu Met Thr Asp Ala Arg Arg Arg
148                565                570                575
149 Val Cys His Thr Glu Asp Phe Gln Lys Glu Glu Gly Thr Val Asn Gly
150                580                585                590
151 Ala Ser Trp His Thr Val Ala Gly Ser Leu Asn Asp Phe Ser Tyr Leu
152                595                600                605
153 His Thr Asn Cys Phe Glu Leu Ser Ile Tyr Val Gly Cys Asp Lys Tyr
154                610                615                620

```

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```

155 Pro His Glu Ser Glu Leu Pro Glu Glu Trp Glu Asn Asn Arg Glu Ser
156 625          630          635          640
157 Leu Ile Val Phe Met Glu Gln Val His Arg Gly Ile Lys Gly Ile Val
158          645          650          655
159 Arg Asp Leu Gln Gly Lys Gly Ile Ser Asn Ala Val Ile Ser Val Glu
160          660          665          670
161 Gly Val Asn His Asp Ile Arg Thr Ala Ser Asp Gly Asp Tyr Trp Arg
162          675          680          685
163 Leu Leu Asn Pro Gly Glu Tyr Val Val Thr Ala Lys Ala Glu Gly Phe
164          690          695          700
165 Ile Thr Ser Thr Lys Asn Cys Met Val Gly Tyr Asp Met Gly Ala Thr
166 705          710          715          720
167 Arg Cys Asp Phe Thr Leu Thr Lys Thr Asn Leu Ala Arg Ile Arg Glu
168          725          730          735
169 Ile Met Glu Thr Phe Gly Lys Gln Pro Val Ser Leu Pro Ser Arg Arg
170          740          745          750
171 Leu Lys Leu Arg Gly Arg Lys Arg Arg Gln Arg Gly
172          755          760
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 200
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Targeting Vector
183 <400> SEQUENCE: 3
184 ggcacatggccc gtctggggac cgcctgccct gcgctggcgc tggccctggc acttgtggcg 60
185 gtggccctgg ctggagtcag agcccagggc gcagccttcg aggagcctga ctattacagc 120
186 caggagctct ggcggcgcgg gcgctattat gggcatccgg agcctgagcc ggagccggag 180
187 ctcttctcgc cttcaatgca
188          200
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 200
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: Targeting Vector
197 <400> SEQUENCE: 4
198 gagggagaag ttagttgcag agacgcctcc accaggtaac ttttgcacgc ggcagcccga 60
199 gggggcgcca gcgatcgtg cactccaggg gacacctggc ttccagtatg ttttcttgag 120
200 tgagcccagc caaagtcctg tggcgctgt gttattccct agagactaca tctgagctaa 180
201 gttcagcttt ctctccctgc
202          200

```

VERIFICATION SUMMARY

DATE: 05/31/2002

PATENT APPLICATION: US/09/900,518A

TIME: 14:04:01

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\05312002\I900518A.raw

Does Not Comply
Corrected Diskette Needed



OIPE

RAW SEQUENCE LISTING

DATE: 05/23/2002

PATENT APPLICATION: US/09/900,518A

TIME: 17:47:37

Input Set : A:\R-716 sequence listing for submission.txt

Output Set: N:\CRF3\05232002\I900518A.raw

4 <110> APPLICANT: Allen, Keith D.
5 Zhang, Qin
7 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CX2 GENE
8 DISRUPTIONS
10 <130> FILE REFERENCE: R-716
12 <140> CURRENT APPLICATION NUMBER: US 09/900,518A
13 <141> CURRENT FILING DATE: 2001-07-06
15 <150> PRIOR APPLICATION NUMBER: US 60/216,178
16 <151> PRIOR FILING DATE: 2000-07-06
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

189 <210> SEQ ID NO: 4
190 <211> LENGTH: 200
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: Targeting Vector
197 <400> SEQUENCE: 4
198 gagggagaag ttagttgcag agacgcctcc accaggtaac ttttgcacg ggcagcccga 60
199 gggggcgcca gcatcggtg cactccagg gacacctggc ttccagtatg ttttcttgag 120
200 tgagcccagc caaagtcctg tgggtgctgt gttattccct agagactaca tctgagctaa 180
201 gttcagcttt ctctccctgc 200
E--> 205 1

remove extra material from end
of file

VERIFICATION SUMMARY

DATE: 05/23/2002

PATENT APPLICATION: US/09/900,518A

TIME: 17:47:38

Input Set : A:\R-716 sequence listing for submission.txt

Output Set: N:\CRF3\05232002\I900518A.raw

L:205 M:254 E: No. of Bases conflict, this line has no nucleotides.